

## **RAW SEQUENCE LISTING**

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Application Serial Number: **10630555**

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# ***ENTERED***

(1) GENERAL INFORMATION:

- (i) APPLICANT: MIYAZONO, Kohei  
TEN DIJKE, Peter  
FRANZEN, Petra  
YAMASHITA, Hidetoshi  
HELDIN, Carl-Henrik
  - (ii) TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS  
HAVING SERINE THREONINE KINASE DOMAINS,  
AND THEIR USE
  - (iii) NUMBER OF SEQUENCES: 48
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
    - (B) STREET: 666 Fifth Avenue
    - (C) CITY: New York City
    - (D) STATE: New York
    - (E) COUNTRY: USA
    - (F) ZIP: 10103
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
    - (B) COMPUTER: IBM PS/2
    - (C) OPERATING SYSTEM: PC-DOS
    - (D) SOFTWARE: Wordperfect
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: US/09/903,068C
    - (B) FILING DATE: 11-Jul-2001
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: PCT/GB93/02367
    - (B) FILING DATE: November 17, 1993
    - (A) APPLICATION NUMBER: GB 9224057.1
    - (B) FILING DATE: November 17, 1992
    - (A) APPLICATION NUMBER: GB 9304677.9
    - (B) FILING DATE: March 8, 1993
    - (A) APPLICATION NUMBER: GB 9304680.3
    - (B) FILING DATE: March 8, 1993
    - (A) APPLICATION NUMBER: 9311047.6
    - (B) FILING DATE: May 28, 1993
    - (A) APPLICATION NUMBER: 9313763.6
    - (B) FILING DATE: July 2, 1993
    - (A) APPLICATION NUMBER: 9316099.2
    - (B) FILING DATE: August 3, 1993
    - (A) APPLICATION NUMBER: 321344.5
    - (B) FILING DATE: October 15, 1993
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Norman D. Hanson
    - (B) REGISTRATION NUMBER: 30,946
    - (C) REFERENCE/DOCKET NUMBER: LUD 5298.4 DIV (10105901)
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (212) 318-3000
    - (B) TELEFAX: (212) 318-3400
- (2) INFORMATION FOR SEQ ID NO: 1:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1984 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: unknown
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (v) FRAGMENT TYPE: internal
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 283..1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA  
60 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC  
120 GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT  
180 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA  
240 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC  
294  
Met Thr Leu Gly  
1  
TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG  
342 Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln  
5 10 15 20  
GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT  
390 Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys  
25 30 35  
GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA  
438 Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr  
40 45 50  
GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC  
486 Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly  
55 60 65  
TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC  
534 Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe  
70 75 80  
GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC  
582 Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser  
85 90 95 100  
CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT  
630 Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp  
105 110 115  
GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG  
678 Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu  
120 125 130  
GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG  
726 Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu  
135 140 145  
AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG  
774 Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu  
150 155 160  
AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT  
822 Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser  
165 170 175 180  
GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG

[illegible]

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Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
      425      430      435
GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT
1638
Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
      440      445      450
AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG
1686
Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
      455      460      465
CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG
1734
Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
      470      475      480
ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA
1782
Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
      485      490      495      500
GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC
1831
Val Ile Gln
TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG
1891
TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT
1951
ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA
1984

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
  1      5      10      15
Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
      20      25      30
Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
      35      40      45
Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
      50      55      60
Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
      65      70      75      80
Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
      85      90      95
His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
      100      105      110
Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
      115      120      125
Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
      130      135      140
Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
      145      150      155      160
Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
      165      170      175
Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
      180      185      190
Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
      195      200      205

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Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu
	210					215					220				
Ser	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe
225					230					235					240
Arg	Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile
				245					250					255	
Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln
			260					265					270		
Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe
		275					280					285			
Leu	Gln	Arg	Gln	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val
	290					295					300				
Ser	Ala	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr
305					310					315					320
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Arg	Asn	Val
				325					330					335	
Leu	Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala
			340					345					350		
Val	Met	His	Ser	Gln	Gly	Ser	Asp	Tyr	Leu	Asp	Ile	Gly	Asn	Asn	Pro
		355					360					365			
Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Gln
	370					375					380				
Ile	Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala
385					390					395					400
Phe	Gly	Leu	Val	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Thr	Ile	Val	Asn	Gly
				405					410					415	
Ile	Val	Glu	Asp	Tyr	Arg	Pro	Pro	Phe	Tyr	Asp	Val	Val	Pro	Asn	Asp
			420					425					430		
Pro	Ser	Phe	Glu	Asp	Met	Lys	Lys	Val	Val	Cys	Val	Asp	Gln	Gln	Thr
		435					440					445			
Pro	Thr	Ile	Pro	Asn	Arg	Leu	Ala	Ala	Asp	Pro	Val	Leu	Ser	Gly	Leu
	450					455					460				
Ala	Gln	Met	Met	Arg	Glu	Cys	Trp	Tyr	Pro	Asn	Pro	Ser	Ala	Arg	Leu
465					470					475					480
Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Gln	Lys	Ile	Ser	Asn	Ser	Pro
				485					490					495	
Glu	Lys	Pro	Lys	Val	Ile	Gln									
			500												

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2724 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 104..1630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAG  
 60  
 GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA  
 115

Met Val Asp Gly